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<110> Cohen, Daniel
Blumenfeld, Marta
Ilya, Chumakov
Bougueleret, Lydie

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Sequence data from the GEN-T113XC3D2 project, generated by the S. SHARE Sequences GEN-T113XC3D2 Sequences (1st) (DJB) file.

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S. SHARI, Sequences of N-ETHANOL-3D2 Sequences (st.doc) DNB: 111

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Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu Glu Gln Glu			
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ctt ata gaa ttt tat gag tca cca gat cca gaa aga aga aaa aga ttt			918
Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe			
285	290	295	
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Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro			
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tca atg ttg atc tta agt ggt ttg act gca ggc atg ctt atg acc gat			1014
Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu Met Thr Asp			
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<223> Klein, Kanehisa and DeLisi identification method, potential helix

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<223> potential Leucine zipper site, Prosite match

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<222> 350

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		20					25					30			
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	35					40					45				
Ser	Met	Val	Leu	Phe	Phe	Phe	Glu	Asn	Tyr	Thr	Gly	Val	Gln	Ile	Leu
	50				55					60					
Leu	Tyr	Gly	Asp	Leu	Pro	Lys	Asn	Lys	Glu	Asn	Ile	Ile	Tyr	Leu	Ala
65				70					75					80	
Asn	His	Gln	Ser	Thr	Val	Asp	Trp	Ile	Val	Ala	Asp	Ile	Leu	Ala	Ile
		85						90					95		
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		100					105				110				
Lys	Trp	Leu	Pro	Leu	Tyr	Gly	Cys	Tyr	Phe	Ala	Gln	His	Gly	Gly	Ile
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 180 185 190
 Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys Met Lys
 195 200 205
 Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys
 210 215 220
 Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met Thr Glu Phe Leu
 225 230 235 240
 Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys
 245 250 255
 Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu
 260 265 270
 Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro
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 Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys
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 Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu
 305 310 315 320
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<213> Homo sapiens

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 35 40 45
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 50 55 60
 Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu
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 Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala Asn His Gln Ser Thr
 85 90 95
 Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu
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 Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu
 115 120 125
 Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser
 130 135 140
 Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val
 145 150 155 160
 Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg
 165 170 175
 Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala

210	215	220
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	245	250
Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu		255
	260	265
Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys		270
	275	280
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	290	295
Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys		300
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Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu		320
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1 5

<210> 15
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1 5

<210> 16
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<222> 204..212

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Val Glu Tyr Ile Tyr Asp Ile Thr Ile

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<210> 17

<211> 9

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<221> SITE

<222> 271..279

<223> box3 from P38226

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Ile Glu Ser Leu Tyr Asp Ile Thr Ile

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<210> 18

<211> 9

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<221> SITE

<222> 265..273

<223> box3 from Z49770

<400> 18

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1

5

<210> 19

<211> 9

<212> PRT

<213> Homo sapiens

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<221> SITE

<222> 138..146

<223> box3 fromZ49860

<400> 19

Val Pro Ala Ile Tyr Asp Met Thr Val

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5

<210> 20

<220>

<221> SITE

<222> 218..226

<223> box3 from Z29518

<400> 20

Val Pro Ala Ile Tyr Asp Thr Thr Val

1

5

<210> 21

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<223> polymorphic base C

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<222> 1..23
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<221> primer_bind
<222> 25..47
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<223> polymorphic fragment 99-213

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<222> 1..23

<223> potential microsequencing oligo 99-213.mis1

<221> primer_bind

<222> 25..47

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<223> polymorphic base A

<221> primer_bind

<222> 1..23

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<221> primer_bind

<222> 25..47

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<220>
<221> allele
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<221> allele
<222> 24
<223> base T ; C in SEQ ID21

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-123.mis1

<221> primer_bind
<222> 25..47
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<400> 30
tttctcatcc tcacacctca ctgtgccct cctgaaccca ctccttt

47

<210> 31
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<223> polymorphic fragment 4-26, variant version of SEQ ID22

<221> allele
<222> 24
<223> base A ; G in SEQ ID22

<221> primer_bind
<222> 1..23

<223> complement potential microsequencing oligo 4-26.mis2

<400> 31

ccctgtgnaga cacgtcctgt atcattgttg agatgggaaa gtgcatc

47

<210> 32

<211> 47

<212> DNA

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<222> 1..47

<223> polymorphic fragment 4-14, variant version of SEQ ID23

<221> allele

<222> 24

<223> base C ; T in SEQ ID23

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-14.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-14.mis2

<400> 32

gcagggagca gaccagacat gatctgttct agtctagctg attcata

47

<210> 33

<211> 47

<212> DNA

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<221> allele

<222> 24

<223> base G ; C in SEQ ID24

<221> primer_bind

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<223> potential microsequencing oligo 4-77.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-77.mis2

<210> 34
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<221> allele
<222> 24
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<222> 1..23
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<221> primer_bind
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<223> complement potential microsequencing oligo 99-217.mis2

<400> 34
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47

<210> 35
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<221> primer_bind
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<221> primer_bind
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<400> 35
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47

<210> 36
<211> 47

<221> allele
<222> 1..47
<223> polymorphic fragment 99-213, variant version of SEQ ID27

<221> allele
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<221> primer_bind
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<400> 36
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47

<210> 37
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<221> allele
<222> 24
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<221> primer_bind
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<221> primer_bind
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<223> complement potential microsequencing oligo 99-221.mis2

<400> 37
agcttgagaa accagaaaag ccacaaggag gctcctacca catgggt

47

<210> 38
<211> 47
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<220>
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<223> base G ; A in SEQ ID29

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-135.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-135.mis2

<400> 38

agtcactata tctatgttta atggagatag aaagagatgc agaaatg

47

<210> 39

<211> 18

<212> DNA

<213> Homo Sapiens

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18

<210> 40

<211> 18

<212> DNA

<213> Homo Sapiens

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<222> 1..18

<223> upstream amplification primer 4-26-PU

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<210> 41

<211> 18

<212> DNA

<213> Homo Sapiens

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<222> 1..18

<223> upstream amplification primer 4-14-PU

<400> 41

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<212> DNA
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11947

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<210> 43
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34234

<400> 43
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<210> 44
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<400> 44
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<210> 45
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<211> 19
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19

<210> 47
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<400> 47
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18

<210> 48
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18

<210> 49
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<400> 49
tgaggactgc taggaaag

18

<213> Homo Sapiens

<220>

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<222> 1..20

<223> downstream amplification primer 4-14-RP

<400> 50

gactgtatcc tttgatgcac

20

<210> 51

<211> 20

<212> DNA

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123

58 complement

<400> 51

ggaaaggtac tcattcatag

20

<210> 52

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<212> DNA

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<222> 1..21

<223> downstream amplification primer 99-217-RP, extracted from SEQ ID1 34625
34645 complement

<400> 52

gtttattttg tgtgagcttt g

21

<210> 53

<211> 20

<212> DNA

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<222> 1..20

<223> downstream amplification primer 4-67-RP, extracted from SEQ ID1 51996
520

15 complement

<210> 54
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<223> downstream amplification primer 99-213-RP

<400> 54
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<210> 56
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<400> 56
aaacacctcc cattgtgc 18

<210> 57
<211> 47
<212> DNA
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<223> polymorphic fragment 99-1482

<221> allele
<222> 24

<223> potential microsequencing oligo 99-1482.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1482.mis2

<400> 57

agtgaagtct gagggggaaa aatcaaccct atagaggga ggatctg

47

<210> 58

<211> 47

<212> DNA

<213> Homo Sapiens

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<222> 1..47

<223> polymorphic fragment 4-73, extracted from SED ID1 13657 13703

<221> allele

<222> 24

<223> polymorphic base C in PG1 (13680) SEQ ID1

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-73.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-73.mis2

<400> 58

gttttcctta tgatgttaca tggcttattt ttaaaggtaa tgaaaac

47

<210> 59

<211> 47

<212> DNA

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<222> 1..47

<223> polymorphic fragment 4-65, extracted from SEQ ID1 51448 51494

<221> allele

<222> 24

<223> polymorphic base T in PG1 (51471) SEQ ID1

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-65.mis1

<400> 59
ggtgctgctc agcggccttg acgtagactt gctaggaaga aatgcag

47

<210> 60
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<221> allele
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<221> primer_bind
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<221> primer_bind
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<400> 60
agtgaagtct gagggggaaa aataaacct atagaggga ggatctg

47

<210> 61
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<212> DNA
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<221> allele
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<223> base G ; C in SEQ ID58

<221> primer_bind
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<221> primer_bind
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<400> 61
attttcctta tgaattaca tgggttattt ttaaaggtaa tgaaaac

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<212> DNA
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<223> base C ; T in SEQ ID59

<221> primer_bind
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<223> potential microsequencing oligo 4-65.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-65.mis2

<400> 62
ggtgctgctc agcggcttgc acgcagactt gctaggaaga aatgcag 4 /

<210> 63
<211> 21
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<400> 63
atcaaatcag tgaagtctga g 21

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13564

<400> 64
atcgctggaa cattctgg 18

<210> 65

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51168

<400> 65
gatttaagct acgctattag 20

<210> 66
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<400> 66
acaaatctat ataaggctgg 20

<210> 67
<211> 20
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<222> 1..20
<223> downstream amplification primer 4-73-RP, extracted from SEQ ID1 13962
13981 complement

<400> 67
ctcttggtta aacagcagtg 20

<210> 68
<211> 18
<212> DNA
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<223> downstream amplification primer 4-65-RP, extracted from SEQ ID1 51482
51499 complement

<400> 68
tggctctgca tttcttcc 18

<400> 69

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ctgctgtccc tgggtgtcca cacgtactcc atg cgc tac ctg ctg ccc agc gtc      54
                               Met Arg Tyr Leu Leu Pro Ser Val
                               1           5

gtg ctc ctg ggc acg gcg ccc acc tac gtg ttg gcc tgg ggg gtc tgg      102
Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
   10           15           20

cgg ctg ctc tcc gcc ttc ctg ccc gcc cgc ttc tac caa gcg ctg gac      150
Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
  25           30           35           40

gac cgg ctc tac tgc gtc tac cag agc atg gtg ctc ttc ttc ttc gag      198
Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
           45           50           55

aat tac acc ggg gtc cag ata ttg cta tat gga gat ttg cca aaa aat      246
Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu Pro Lys Asn
           60           65           70

aaa gaa aat ata ata tat tta gca aat cat caa agc aca gtt gac tgg      294
Lys Glu Asn Ile Ile Tyr Leu Ala Asn His Gln Ser Thr Val Asp Trp
           75           80           85

att gtt gct gac atc ttg gcc atc agg cag aat gcg cta gga cat gtg      342
Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu Gly His Val
           90           95           100

cgc tac gtg ctg aaa gaa ggg tta aaa tgg ctg cca ttg tat ggg tgt      390
Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu Tyr Gly Cys
  105           110           115           120

tac ttt gct cag cat gga gga atc tat gta aag cgc agt gcc aaa ttt      438
Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe
           125           130           135

aac gag aaa gag atg cga aac aag ttg cag agc tac gtg gac gca gga      486
Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly
           140           145           150

act cca atg tat ctt gtg att ttt cca gaa ggt aca agg tat aat cca      534
Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro
           155           160           165

gag caa aca aaa gtc ctt tca gct agt cag gca ttt gct gcc caa cgt      582
Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg
           170           175           180

ggc ctt gca gta tta aaa cat gtg cta aca cca cga ata aag gca act      630
Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr
  185           190           195           200

cac gtt gct ttt gat tgc atg aag aat tat tta gat gca att tat gat      678
His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp
           205           210           215

gtt acg gtg gtt tat gaa ggg aaa gac gat gga ggg tag cgaagagagt      727
Val Thr Val Val Tyr Glu Gly Lys Asp Asp Gly Gly *
           220           225

caccgaccat gacggaattt ctctgcaaag aatgtccaaa aattcatatt cacattgac      787
gtatcgacaa aaaagatgtc ccagaagaac aagaacatat gagaagatgg ctgcatgaac      847
gtttcgaaat caaagataag atgcttatag aattttatga gtcaccagat ccagaaagaa      907
gaaaaagatt tcttgggaaa agtggttaatt ccaaattaag tatcaagaag actttaccat      967
caatgttgat cttaagtggg ttgactgcag gcatgcttat gaccgatgct ggaaggaagc     1027
tgtatgtgaa cacctggata tatggaaccc tacttggtctg cctgtggggtt actattaaag     1087
cataqacaaq tagctgtctc cagacagtgg gatgtgctac attgtctatt tttggcggct     1147

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ctgaagtact tctaataatac tgaggggaagt ataatatgtg gaacaaaactc tcaacaaaat 4927
gtttattgat gttgatgaaa cagatcagtt tttccatccg gattattatt ggttcatgat 4987
tttataatgtg aatatgtaag atatgttctg caattttata aatgttcatg tcttttttta 5047
aaaaagggtgc tatcgaaatt ctgtgtctcc agcaggcaag aatacttgac taactctttt 5107
tgtctcttta tggatattttc agaataaagt ctgacttgtg tttttgagat tattgggtgcc 5167
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<211> 228

<212> PRT

<213> Homo sapiens

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Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
          20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
          50          55          60
Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
65          70          75          80
Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
          85          90          95
Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
          100          105          110
Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
          115          120          125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
          130          135          140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
145          150          155          160
Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
          165          170          175
Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys His Val
          180          185          190
Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys Met Lys
          195          200          205
Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys
          210          215          220
Asp Asp Gly Gly
225

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<210> 71

<211> 158

<212> DNA

<213> Homo sapiens

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acgatggagg gtagcgaaga gattcaccga ccatgacg 158

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<213> Mus musculus

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<222> 740..758

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                                     Met Arg Tyr Leu
                                     1
ctc ccc agc gtc ctg ttg ctg ggc tgc gcg ccc acc tac ctg ctg gcc      104
Leu Pro Ser Val Leu Leu Leu Gly Ser Ala Pro Thr Tyr Leu Leu Ala
5          10          15          20
tgg acg ctg tgg cgg gtg ctc tcc gcg ctg atg ccc gcc cgc ctg tac      152
Trp Thr Leu Trp Arg Val Leu Ser Ala Leu Met Pro Ala Arg Leu Tyr
25          30          35
cag cgc gtg gac gac cgg ctt tac tgc gtc tac cag aac atg gtg ctc      200
Gln Arg Val Asp Asp Arg Leu Tyr Cys Val Tyr Gln Asn Met Val Leu
40          45          50
ttc ttc ttc gag aac tac acc ggg gtc cag ata ttg cta tat gga gat      248
Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp
55          60          65
ttg cca aaa aat aaa gaa aat gta ata tat cta gcg aat cat caa agc      296
Leu Pro Lys Asn Lys Glu Asn Val Ile Tyr Leu Ala Asn His Gln Ser
70          75          80
aca gtt gac tgg att gtt gcg gac atg ctg gct gcc aga cag gat gcc      344
Thr Val Asp Trp Ile Val Ala Asp Met Leu Ala Ala Arg Gln Asp Ala
85          90          95          100
cta gga cat gtg cgc tac gta ctg aaa gac aag tta aaa tgg ctt ccg      392
Leu Gly His Val Arg Tyr Val Leu Lys Asp Lys Leu Lys Trp Leu Pro
105          110          115
ctg tat ggg ttc tac ttt gct cag cat gga gga att tat gta aaa cga      440
Leu Tyr Gly Phe Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg
120          125          130
agt gcc aaa ttt aat gat aaa gaa atg aga agc aag ctg cag agc tat      488
Ser Ala Lys Phe Asn Asp Lys Glu Met Arg Ser Lys Leu Gln Ser Tyr
135          140          145
gtg aac gca gga aca ccg atg tat ctt gtg att ttc cca gag gga aca      536
Val Asn Ala Gly Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr
150          155          160
agg tat aat gca aca tac aca aaa ctc ctt tca gcc agt cag gca ttt      584
Arg Tyr Asn Ala Thr Tyr Thr Lys Leu Leu Ser Ala Ser Gln Ala Phe
165          170          175          180
gct gct cag cgg ggc ctt gca gta tta aaa cac gta ctg aca cca aga      632
Ala Ala Gln Arg Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg
185          190          195
ata aag gcc act cac gtt gct ttt gat tct atg aag agt cat tta gat      680
Ile Lys Ala Thr His Val Ala Phe Asp Ser Met Lys Ser His Leu Asp
200          205          210

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Gly	Lys	Tyr	Ser	Asn	Pro	Pro	Ser	Met	Thr	Glu	Phe	Leu	Cys	Lys	Gln	
230						235					240					
tgc	cca	aaa	ctt	cat	att	cac	ttt	gat	cgt	ata	gac	aga	aat	gaa	gtt	824
Cys	Pro	Lys	Leu	His	Ile	His	Phe	Asp	Arg	Ile	Asp	Arg	Asn	Glu	Val	
245					250					255				260		
cca	gag	gaa	caa	gaa	cac	atg	aaa	aag	tgg	ctt	cat	gag	cgc	ttt	gag	872
Pro	Glu	Glu	Gln	Glu	His	Met	Lys	Lys	Trp	Leu	His	Glu	Arg	Phe	Glu	
				265					270					275		
ata	aaa	gat	agg	ttg	ctc	ata	gag	ttc	tat	gat	tca	cca	gat	cca	gaa	920
Ile	Lys	Asp	Arg	Leu	Leu	Ile	Glu	Phe	Tyr	Asp	Ser	Pro	Asp	Pro	Glu	
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Leu	Met	Thr	Asp	Ala	Gly	Arg	Lys	Leu	Tyr	Val	Asn	Thr	Trp	Ile	Tyr		
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Ile Phe Thr Leu Ile Val Ser Thr Lys Lys Met Ser Gln Lys Asn Lys			
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Asn Ile *			
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
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Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
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<211> 77

<212> PRT

<213> Homo sapiens

<400> 125

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20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Leu Thr
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<400> 126
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 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln His Gly
 50 55 60
 Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg
 65 70 75 80
 Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val
 85 90 95
 Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu
 100 105 110
 Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Glu Phe Leu Cys Lys Glu
 115 120 125
 Cys Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val
 130 135 140
 Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu
 145 150 155 160
 Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu
 165 170 175
 Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile
 180 185 190
 Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly
 195 200 205
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 Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala
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<210> 127
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 <212> PFT
 <213> Homo sapiens

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 <223> Box II

<221> SITE
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35           40           45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln His Gly
50           55           60
Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg
65           70           75           80
Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val
85           90           95
Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu
100          105          110
Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys
115          120          125
His Val Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys
130          135          140
Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu
145          150          155          160
Gly Lys Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met Thr Glu
165          170          175
Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp Arg Ile
180          185          190
Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu
195          200          205
His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu
210          215          220
Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn
225          230          235          240
Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser
245          250          255
Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr
260          265          270
Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr
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<210> 128
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<221> SITE
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<400> 128

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 65 70 75 80
 Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val
 85 90 95
 Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe
 100 105 110
 Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val
 115 120 125
 Tyr Glu Gly Lys Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met
 130 135 140
 Thr Glu Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp
 145 150 155 160
 Arg Ile Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg
 165 170 175
 Trp Leu His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe
 180 185 190
 Tyr Glu Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser
 195 200 205
 Val Asn Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile
 210 215 220
 Leu Ser Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys
 225 230 235 240
 Leu Tyr Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp
 245 250 255
 Val Thr Ile Lys Ala
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<210> 129

<211> 90

<212> PRT

<213> Homo sapiens

<400> 129

Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
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 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Asn Phe
 50 55 60
 Ser Ala Lys Asn Val Gln Lys Phe Ile Phe Thr Leu Ile Val Ser Thr
 65 70 75 80
 Lys Lys Met Ser Gln Lys Asn Lys Asn Ile
 85 90

<210> 130

<211> 68

<212> PRT

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 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Asp Ala
 50 55 60
 Tyr Arg Ile Leu
 65

<210> 131
 <211> 66
 <212> PRT
 <213> Homo sapiens
 <400> 131

Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
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 20 25 30
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Arg Leu
 50 55 60
 Asp Ser
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<210> 132
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> 81..83
 <223> Box I

<400> 132
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 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
 50 55 60
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 65 70 75 80
 Asn His Gln Ser Thr Asp Val Ser Cys Asp Phe Ser Arg Arg Tyr Lys
 85 90 95
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<210> 133

<220>

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<222> 81..83

<223> Box I

<400> 133

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
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Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
50          55          60
Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
65          70          75          80
Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
85          90          95
Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
100         105         110
Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
115         120         125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
130         135         140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Asn Phe Ser Ala Lys Asn
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Val Gln Lys Phe Ile Phe Thr Leu Ile Val Ser Thr Lys Lys Met Ser
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Gln Lys Asn Lys Asn Ile
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<210> 134

<211> 315

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 81..83

<223> Box I

<221> SITE

<222> 160..165

<223> Box II

<400> 134

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
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20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu

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<210> 135
<211> 300
<212> PRT
<213> Homo sapiens
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<223> Box II
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1400> 135
Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1          5          10          15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
50          55          60

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Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
      100                      105                      110
Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
      115                      120                      125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
      130                      135                      140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
      145                      150                      155                      160
Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
      165                      170                      175
Ser Gln Ala Phe Ala Ala Gln Arg Glu Phe Leu Cys Lys Glu Cys Pro
      180                      185                      190
Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu
      195                      200                      205
Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys
      210                      215                      220
Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg
      225                      230                      235                      240
Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys
      245                      250                      255
Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu
      260                      265                      270
Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly
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Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala
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Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
      20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
      35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
      50          55          60
Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
      65          70          75          80
Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile

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115	120	125
Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys		
130	135	140
Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe		
145	150	155
Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala		
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Ser Gln Ala Phe Ala Ala Gln Arg Gly		175
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agt	gcc	aaa	ttt	aat	gat	aaa	gaa	atg	aga	agc	aag	ctg	cag	agc	tat	488
Ser	Ala	Lys	Phe	Asn	Asp	Lys	Glu	Met	Arg	Ser	Lys	Leu	Gln	Ser	Tyr	
		135					140					145				
gtg	aac	gca	gga	aca	ccg	atg	tat	ctt	gtg	att	ttc	cca	gag	gga	aca	536
Val	Asn	Ala	Gly	Thr	Pro	Met	Tyr	Leu	Val	Ile	Phe	Pro	Glu	Gly	Thr	
		150					155				160					
agg	tat	aat	gca	aca	tac	aca	aaa	ctc	ctt	tca	gcc	agt	cag	gca	ttt	584
Arg	Tyr	Asn	Ala	Thr	Tyr	Thr	Lys	Leu	Leu	Ser	Ala	Ser	Gln	Ala	Phe	
					170					175					180	
gct	gct	cag	cgg	ggc	ctt	gca	gta	tta	aaa	cac	gta	ctg	aca	cca	aga	632
Ala	Ala	Gln	Arg	Gly	Leu	Ala	Val	Leu	Lys	His	Val	Leu	Thr	Pro	Arg	
				185					190					195		
ata	aag	gcc	act	cac	ggt	gct	ttt	gat	tct	atg	aag	agt	cat	tta	gat	680
Ile	Lys	Ala	Thr	His	Val	Ala	Phe	Asp	Ser	Met	Lys	Ser	His	Leu	Asp	
			200					205					210			
gca	att	tat	gat	gtc	aca	gtg	ggt	tat	gaa	ggg	aat	gag	aaa	ggt	tca	728
Ala	Ile	Tyr	Asp	Val	Thr	Val	Val	Tyr	Glu	Gly	Asn	Glu	Lys	Gly	Ser	
		215					220					225				
gga	aaa	tac	tca	aat	cca	cca	tcc	atg	act	gag	ttt	ctc	tgc	aaa	cag	776
Gly	Lys	Tyr	Ser	Asn	Pro	Pro	Ser	Met	Thr	Glu	Phe	Leu	Cys	Lys	Gln	
		230				235					240					
tgc	cca	aaa	ctt	cat	att	cac	ttt	gat	cgt	ata	gac	aga	aat	gaa	ggt	824
Cys	Pro	Lys	Leu	His	Ile	His	Phe	Asp	Arg	Ile	Asp	Arg	Asn	Glu	Val	
					250				255					260		
cca	gag	gaa	caa	gaa	cac	atg	aaa	aag	tgg	ctt	cat	gag	cgc	ttt	gag	872
Pro	Glu	Glu	Gln	Glu	His	Met	Lys	Lys	Trp	Leu	His	Glu	Arg	Phe	Glu	
				265					270					275		
ata	aaa	gat	agg	ttg	ctc	ata	gag	ttc	tat	gat	tca	cca	gat	cca	gaa	920
Ile	Lys	Asp	Arg	Leu	Leu	Ile	Glu	Phe	Tyr	Asp	Ser	Pro	Asp	Pro	Glu	
			280					285					290			
aga	aga	aac	aaa	ttt	cct	ggg	aaa	agt	ggt	cat	tcc	aga	cta	agt	gtg	968
Arg	Arg	Asn	Lys	Phe	Pro	Gly	Lys	Ser	Val	His	Ser	Arg	Leu	Ser	Val	
		295					300					305				
aag	aag	act	tta	cct	tca	gtg	ttg	atc	ttg	ggg	agt	ttg	act	gcg	gtc	1016
Lys	Lys	Thr	Leu	Pro	Ser	Val	Leu	Ile	Leu	Gly	Ser	Leu	Thr	Ala	Val	
		310					315				320					
atg	ctg	atg	acg	gag	tcc	gga	agg	aaa	ctg	tac	atg	ggc	acc	tgg	ttg	1064
Met	Leu	Met	Thr	Glu	Ser	Gly	Arg	Lys	Leu	Tyr	Met	Gly	Thr	Trp	Leu	
				325		330				335				340		
tat	gga	acc	ctc	ctt	ggc	tgc	ctg	tgg	ttt	ggt	att	aaa	gca	taa		1109

taagccttga tgattgaaca ctggataaag tcgagtcttg tgaccacagc caacatgcat 1289
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<222> 25..47

<223> complement potential microsequencing oligo 4-84-262.mis2

<400> 223

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<222> 14

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<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-86-206.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-86-206.mis2

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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 4-86-309.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-86-309.mis2

<400> 225
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<221> allele
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<223> polymorphic base G

<221> primer_bind
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<223> potential microsequencing oligo 4-88-349.mis1

<221> primer_bind
<222> 25..47
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<400> 226
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<210> 227
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<221> allele
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<221> primer_bind
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<221> primer_bind
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<400> 227
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<223> polymorphic fragment 99-123-184

<221> allele
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<223> polymorphic base G

<221> primer_bind
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<223> potential microsequencing oligo 99-123-184.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-123-184.mis2

<400> 228
ccagcccaga acattcacca gctggggccaa gagttctgct gggtttt

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<210> 229
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<221> primer_bind
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<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-128-202.mis2

<400> 229
aatgtctgtt tcttagagaa ctgaaacaca cacacatata tacacac 47

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<221> allele
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<221> primer_bind
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<221> primer_bind
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<400> 230
acaccctac ctcacatgtg tagacaaatg tatgcatata tgtctct 47

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<221> allele
<222> 24
<223> polymorphic base A

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-128-313.mis2

<400> 231
tatgtctcta gacagatata cataagattc tatttgcat agaaaaa 47

<210> 232
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<221> allele
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<223> polymorphic base C

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-128-60.mis1

<221> primer_bind
<222> 25..47
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<400> 232
gcactgtgac ccaggcgcta ggtccctctt acagtgcac tccgaca 47

<210> 233
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<221> allele
<222> 24
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-12907-295.mis1

<221> primer_bind
<222> 25..47

gctatatggc attatatctc cacagggcag acctgatgta caagatg

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<210> 234
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-130-58.mis1

<221> primer_bind
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<400> 234
aaagcaaaag agcttcaaaa atacttcagg agtgtgcata tggcgag

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<210> 235
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<223> polymorphic fragment 99-134-362

<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-134-362.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-134-362.mis2

<400> 235
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<213> Homo Sapiens

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<222> 1..47

<223> polymorphic fragment 99-140-130

<221> allele

<222> 24

<223> polymorphic base C

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<222> 1..23

<223> potential microsequencing oligo 99-140-130.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-140-130.mis2

<400> 236

tgttcaaaag cagctacaga ccacatgtaa acaattgagc atggctg

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<210> 237

<211> 47

<212> DNA

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<222> 1..47

<223> polymorphic fragment 99-1462-238

<221> allele

<222> 24

<223> polymorphic base G

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1462-238.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1462 238.mis2

<400> 237

ccctttcaag gttagtaact catgtgctgt gtttctgctt cagaagg

47

<210> 238

<211> 47

<212> DNA

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<222> 1..47

<223> polymorphic fragment 99-1462-238

<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-147-181.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-147-181.mis2

<400> 238
gtgtcatgaa aaagagcatg ataaaaagaa aaacttaaata ctttata

47

<210> 239
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<223> polymorphic fragment 99-1474-156

<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-1474-156.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-1474-156.mis2

<400> 239
cttgactca taagttaaata attgataaca agaagaaata tggactt

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<210> 240
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<221> allele
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<222> 1..23
<223> potential microsequencing oligo 99-1474-359.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-1474-359.mis2

<400> 240
aaaaaaaatc aaattattgt accaaattcc ctaatatcag atgtgta 47

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<223> polymorphic fragment 99-1479-158

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<223> polymorphic base C

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1479-158.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1479-158.mis2

<400> 241
tttaaaaatc cacttgtaat cgccgctaatt tggagtgtat attcagg 47

<210> 242
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<223> polymorphic fragment 99-1479-379

<221> allele
<222> 24
<223> polymorphic base A

<221> primer_bind
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<400> 242
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<223> polymorphic fragment 99-148-129

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<221> primer_bind
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<223> potential microsequencing oligo 99-148-129.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-148-129.mis2

<400> 243
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<210> 244
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<220>
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<223> potential microsequencing oligo 99-148-132.mis1

<221> primer_bind
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<400> 244
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<211> 47
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-139.mis1

<221> primer_bind
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<400> 245
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<210> 246
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<212> DNA
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<223> polymorphic fragment 99-148-140

<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-148-140.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-148-140.mis2

<400> 246
acaaataatt ttgaatttaa tacatagggc tgcaaaacaa gggtgat 47

<210> 247
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<222> 1..47
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-182.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-182.mis2

<400> 247
ttgatgttga tatgggcaac tgtatgttgg atgggcccaa agcattc

47

<210> 248
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<212> DNA
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<222> 1..47
<223> polymorphic fragment 99-148-366

<221> allele
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<223> polymorphic base G

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-366.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-366.mis2

<400> 248
tccttgtaaa aggtctctcc ctggtgctca cggctgccgc ctcaaag

47

<210> 149
<211> 47
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<223> polymorphic fragment 99-148-76

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-76.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-76.mis2

<400> 249
tgatagaatg ccttcttgaa ttactactct tgatggcttc ataaaaac

47

<210> 250
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<221> primer_bind
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<223> potential microsequencing oligo 99-1480-290.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1480-290.mis2

<400> 250
tgcaccatct tcaccacaac cccgggcaac cactgatcct ttacttg

47

<210> 251
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<220>
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<223> polymorphic fragment 99-1481-285

<221> allele
<222> 24
<223> polymorphic base G

<221> primer_bind
<222> 1..23

<222> 25..47

<223> complement potential microsequencing oligo 99-1481-285.mis2

<400> 251

tcccataacc tgtttttgctt ctcgctctaa cctcaagatg gtataaa

47

<210> 252

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

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<222> 1..47

<223> polymorphic fragment 99-1484-101

<221> allele

<222> 24

<223> polymorphic base A

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1484-101.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1484-101.mis2

<400> 252

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<210> 253

<211> 47

<212> DNA

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<222> 1..47

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<222> 24

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<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1484-328.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1484-328.mis2

<210> 254
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-1485-251.mis1

<221> primer_bind
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<400> 254
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47

<210> 255
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<221> allele
<222> 24
<223> polymorphic base C

<221> primer_bind
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<223> potential microsequencing oligo 99-1490-381.mis1

<221> primer_bind
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<400> 255
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47

<210> 256
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-1493-280.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1493-280.mis2

<400> 256
ggatgacaga gtattgttgg aggaatgggg tttggctgct tgttttt 47

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<223> polymorphic fragment 99-151-94

<221> allele
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<223> polymorphic base A

<221> primer_bind
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<223> potential microsequencing oligo 99-151-94.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-151-94.mis2

<400> 257
attgagatca ttgataagga aatattctaa aatttcaaaa tctatat 47

<210> 258
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<212> DNA
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<220>
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<222> 24
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<221> primer_bind
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<223> potential microsequencing oligo 99-211-291.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-211-291.mis2

<400> 258
ctgggttatat cagactgacc ttcattgtttt caacagggtca atgcctt 47

<210> 259
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<223> polymorphic fragment 99-213-37

<221> allele
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<223> polymorphic base T

<221> primer_bind
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<223> potential microsequencing oligo 99-213-37.mis1

<221> primer_bind
<222> 24..45
<223> complement potential microsequencing oligo 99-213-37.mis2

<400> 259
gtgcttcagg ctgcaggact gttggaggac tccagtgtct gacag 45

<210> 260
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<223> polymorphic fragment 99-221-442

<221> allele
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<221> primer_bind
<222> 25..47
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<400> 260
tgcctttgta gatatgcatg ggaattccat gacctagcca gacgaat 47

<210> 261
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<223> polymorphic fragment 99-222-109

<221> allele
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<223> polymorphic base C

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-222-109.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-222-109.mis2

<400> 261
caggtgagga gtgctggatt ggccacgata tgaatttctt cagcagt 47

<210> 262
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<212> DNA
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<220>
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<221> allele
<222> 24
<223> base G ; A in SEQ ID185

<221> primer_bind
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<221> primer_bind

ctaaacaacc accaaatgca tacggcaacc aggcaaatgc ctgatag

47

<210> 263
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<220>
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<223> polymorphic fragment 4-14-317, variant version of SEQ ID186

<221> allele
<222> 24
<223> base G ; A in SEQ ID186

<221> primer_bind
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<223> potential microsequencing oligo 4-14-317.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-14-317.mis2

<400> 263
cataacatgc aaggtgggca agagaaagag gtgggcacag ctcatga

47

<210> 264
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<212> DNA
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<220>
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<221> allele
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<223> base T ; C in SEQ ID187

<221> primer_bind
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<221> primer_bind
<222> 25..47
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<400> 264
atccaacaca gaaaccgcta aaatcaggca gaagctgtct gcagaga

47

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-20-149, variant version of SEQ ID188

<221> allele

<222> 24

<223> base T ; C in SEQ ID188

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-20-149.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-20-149.mis2

<400> 265

tttttgctgt gtcttcaaag tgattcttgg tttattgcct gctaagg

47

<210> 266

<211> 47

<212> DNA

<213> Homo Sapiens

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<222> 1..47

<223> polymorphic fragment 4-20-77, variant version of SEQ ID189

<221> allele

<222> 24

<223> base T ; A in SEQ ID189

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-20-77.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-20-77.mis2

<400> 266

tgcaacatga agattctgaa gggctcttgg tgtctgagaa cacatct

47

<210> 267

<211> 47

<212> DNA

<213> Homo Sapiens

<221> allele
<222> 24
<223> base C ; A in SEQ ID190

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-22-174.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-22-174.mis2

<400> 267
ggattgtgca gaagttgcct ttctgttca aaaatgtaa tttgttt

47

<210> 268
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<212> DNA
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<220>
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<221> allele
<222> 24
<223> base G ; A in SEQ ID191

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-22-176.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-22-176.mis2

<400> 268
attgtgcaga agttgccttt catgttcaaa aatgttaatt tgtttgt

47

<210> 269
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<220>
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<221> allele

<222> 1..23
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<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-26-60.mis2

<400> 269
gatgggaaag tgcattcttaa gacgggtagc aggccaagga gcgactt 47

<210> 270
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<220>
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<223> polymorphic fragment 4-26-72, variant version of SEQ ID193

<221> allele
<222> 24
<223> base G ; A in SEQ ID193

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-26-72.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-26-72.mis2

<400> 270
catcttaaga cagtttagcag gccgaggagc gacttttaaag ggtgagc 47

<210> 271
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<221> allele
<222> 24
<223> base G ; A in SEQ ID194

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-3-130.mis1

<400> 271
tattgggcct aaaacagtat tctgtaaagc ttaaattggt attaaact

47

<210> 272
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 4-38-63, variant version of SEQ ID195

<221> allele
<222> 24
<223> base G ; A in SEQ ID195

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-38-63.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-38-63.mis2

<400> 272
tataagttat aagaaaatca ggcggaggct aaactttttt tttgttt

47

<210> 273
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<212> DNA
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<220>
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<222> 1..47
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<221> allele
<222> 24
<223> base T ; G in SEQ ID196

<221> primer_bind
<222> 1..23
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<221> primer_bind
<222> 25..47
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<400> 273

<211> 47
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<221> allele
<222> 24
<223> base T ; C in SEQ ID197

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-4-152.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-4-152.mis2

<400> 274
tacttttccca ttgttctga ctttggtatc ctatatataa acagaaa

47

<210> 275
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<220>
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<223> polymorphic fragment 4-4-187, variant version of SEQ ID198

<221> allele
<222> 24
<223> base T ; A in SEQ ID198

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-4-187.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-4-187.mis2

<400> 275
tataaacaga aacatggatg agttaaaaaa aaaaaaaaaa aaaaaaa

47

<210> 276
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<212> DNA

<222> 1..47
<223> polymorphic fragment 4-4-288, variant version of SEQ ID199

<221> allele
<222> 24
<223> base C ; G in SEQ ID199

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-4-288.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-4-288.mis2

<400> 276
ctgtcatcaa ctaattttca caactaccta tgttttgatt tcatgta

47

<210> 277
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<220>
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<221> allele
<222> 24
<223> base T ; C in SEQ ID200

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-42-304.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-42-304.mis2

<400> 277
attattttaa actattttatg taatcttatt ttcagggggtt tttaatt

47

<210> 278
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<220>
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<223> polymorphic fragment 4-42-401, variant version of SEQ ID201

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-42-401.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-42-401.mis2

<400> 278
taagaaagaa ttctgtgttc tggccaaagt ttaaaccac agagcca

47

<210> 279
<211> 47
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<220>
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<221> allele
<222> 24
<223> base T ; C in SEQ ID202

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-43-328.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-43-328.mis2

<400> 279
agaattctgt gttctggcca aagtttaaac ccacagagcc agtttaa

47

<210> 280
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<220>
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<222> 1..47
<223> polymorphic fragment 4-43-70, variant version of SEQ ID203

<221> allele
<222> 24
<223> base C ; G in SEQ ID203

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-43-70.mis2

<400> 280

atgcctcca ttattctcaa aaacaccatg ggacacaaca caagaag

47

<210> 281

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-50-209, variant version of SEQ ID204

<221> allele

<222> 24

<223> base T ; C in SEQ ID204

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-50-209.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-50-209.mis2

<400> 281

atatagagtg tgcattcctg acattgaaac tgaaggcttt atgggtt

47

<210> 282

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

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<222> 1..47

<223> polymorphic fragment 4-50-293, variant version of SEQ ID205

<221> allele

<222> 24

<223> base T ; G in SEQ ID205

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-50-293.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-50-293.mis2

<210> 283
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<220>
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<223> polymorphic fragment 4-50-323, variant version of SEQ ID206

<221> allele
<222> 24
<223> base T ; C in SEQ ID206

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-50-323.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-50-323.mis2

<400> 283
ttttaaacaat tgatgaatct ttattactac aaaaggggttc gatttag

47

<210> 284
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<212> DNA
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<220>
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<223> polymorphic fragment 4-50-329, variant version of SEQ ID207

<221> allele
<222> 24
<223> base T ; C in SEQ ID207

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4 50 329.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-50-329.mis2

<400> 284
acattgatga atctttatta ctataaaagg gttcgattta ggctagc

47

<210> 285

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 4-50-330, variant version of SEQ ID208

<221> allele
<222> 24
<223> base T ; A in SEQ ID208

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-50-330.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-50-330.mis2

<400> 285
cattgatgaa tctttattac tactaaaggg ttcgatttag gctagcc

47

<210> 286
<211> 47
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<220>
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<223> polymorphic fragment 4-52-163, variant version of SEQ ID209

<221> allele
<222> 24
<223> base C ; A in SEQ ID209

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-52-163.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-52-163.mis2

<400> 286
gaacaggata ttcttaacta ccacagaatt ttacacatct attgttt

47

<210> 287
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47

<222> 24
<223> base T ; C in SEQ ID210

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-52-88.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-52-88.mis2

<400> 287
tccatgtcat tattattcaa aagtttaaaa aatacacaag gtgaaaa 47

<210> 288
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 4-53-258, variant version of SEQ ID211

<221> allele
<222> 24
<223> base G ; A in SEQ ID211

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-53-258.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-53-258.mis2

<400> 288
gagaaatcat gcagagagaa tgcgttctca ctcaaatttt aacctaa 47

<210> 289
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 4-54-283, variant version of SEQ ID212

<221> allele
<222> 24
<223> base T ; A in SEQ ID212

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-54-283.mis2

<400> 289
aagtagtttt tcacactttc tctttgatac aatcgatggc ttaatct

47

<210> 290
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 4-54-388, variant version of SEQ ID213

<221> allele
<222> 24
<223> base C ; A in SEQ ID213

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-54-388.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-54-388.mis2

<400> 290
ctctctatcg tatacatctt tacccacgct gcagcgccaa gactcca

47

<210> 291
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 4-55-70, variant version of SEQ ID214

<221> allele
<222> 24
<223> base T ; A in SEQ ID214

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-55-70.mis1

<221> primer_bind
<222> 25..47

tattaagaac ctaggtttta aaatactctc tatcgtatac atctttta

47

<210> 292

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

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<222> 1..47

<223> polymorphic fragment 4-55-95, variant version of SEQ ID215

<221> allele

<222> 24

<223> base C ; A in SEQ ID215

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-55-95.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-55-95.mis2

<400> 292

ctctctatcg tatacatctt tacccacgct gcagcgccaa gactcca

47

<210> 293

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-56-159, variant version of SEQ ID216

<221> allele

<222> 24

<223> base T ; C in SEQ ID216

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-56-159.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-56-159.mis2

<400> 293

aagttttcct tctcttctgt agatgtctcc atgttacagt caactat

47

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-56-213, variant version of SEQ ID217

<221> allele

<222> 24

<223> base G ; A in SEQ ID217

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-56-213.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-56-213.mis2

<400> 294

atggctcatg ttcactctgg ttcgccttca gaggagtgtg atatattt

47

<210> 295

<211> 47

<212> DNA

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<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-58-289, variant version of SEQ ID218

<221> allele

<222> 24

<223> base C ; G in SEQ ID218

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-58-289.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4 58 289.mis2

<400> 295

ataacttgca gcctgctttt ggtcaggggt gactacttta cctgcaa

47

<210> 296

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-58-318.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-58-318.mis2

<400> 296
tgactacttt acctgcaata tttctttgca agtttatttc ttccttt

47

<210> 297
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<220>
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<221> allele
<222> 24
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-60-266.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-60-266.mis2

<400> 297
aacaggacca agacactgca ttatataaag tttcagtatt tcttagc

47

<210> 298
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<221> allele

<222> 1..23

<223> potential microsequencing oligo 4-60-293.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-60-293.mis2

<400> 298

aagttttcagt atttcttagc agatgaagcc agcaggaagt cctccta

47

<210> 299

<211> 47

<212> DNA

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<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-84-241, variant version of SEQ ID222

<221> allele

<222> 24

<223> base T ; G in SEQ ID222

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-84-241.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-84-241.mis2

<400> 299

gaaaaaaaaa tagtgactgc cactgtgaat aattcagttc ttcagaa

47

<210> 300

<211> 47

<212> DNA

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<220>

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<222> 1..47

<223> polymorphic fragment 4-84-262, variant version of SEQ ID223

<221> allele

<222> 24

<223> base G ; A in SEQ ID223

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-84-262.mis1

<400> 300
acggtgaata attcagttct tcagaagcag caacatgac tcatgga

47

<210> 301
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<220>
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 4-86-206.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-86-206.mis2

<400> 301
gtattcaaat caggacacac cacgaatggc atctacacgt taacatt

47

<210> 302
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<220>
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<221> allele
<222> 24
<223> base T ; A in SEQ ID225

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-86-309.mis1

<221> primer_bind
<222> 25..47
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<400> 302

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<220>
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<221> allele
<222> 24
<223> base C ; G in SEQ ID226

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-88-349.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-88-349.mis2

<400> 303
gaaactaaaa gacaatatc agtctgagat tttccaagtt ctttatg

47

<210> 304
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<220>
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-89-87.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4 89 87.mis2

<400> 304
ttcttcctg aacgctgggt tcatatagtt tttgtgtga gaataga

47

<210> 305
<211> 47
<212> DNA

<222> 1..47
<223> polymorphic fragment 99-123-184, variant version of SEQ ID228

<221> allele
<222> 24
<223> base C ; G in SEQ ID228

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-123-184.mis1

<221> primer_bind
<222> 25..47
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<400> 305
ccagcccaga acattcacca gctcggccaa gagttctgct gggtttt

47

<210> 306
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 99-128-202, variant version of SEQ ID229

<221> allele
<222> 24
<223> base C ; A in SEQ ID229

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-128-202.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-128-202.mis2

<400> 306
aatgtctggt ttcttagagaa ctgcaacaca cacacatata tacacac

47

<210> 307
<211> 47
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<223> polymorphic fragment 99-128-275, variant version of SEQ ID230

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-128-275.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-128-275.mis2

<400> 307
acaccctac ctcacatgtg taggcaaag tatgcatata tgtctct

47

<210> 308
<211> 47
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<220>
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<222> 1..47
<223> polymorphic fragment 99-128-313, variant version of SEQ ID231

<221> allele
<222> 24
<223> base G ; A in SEQ ID231

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-128-313.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-128-313.mis2

<400> 308
tatgtctcta gacagatata catgagattc tatttggcat agaaaaa

47

<210> 309
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 99-128-60, variant version of SEQ ID232

<221> allele
<222> 24
<223> base T ; C in SEQ ID232

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-128-60.mis2

<400> 309

gcactgtgac ccaggcgcta gggtcctctt acagtgcac tccgaca

47

<210> 310

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<212> DNA

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<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-12907-295, variant version of SEQ ID233

<221> allele

<222> 24

<223> base G ; A in SEQ ID233

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-12907-295.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-12907-295.mis2

<400> 310

gctatatggc attatatctc cacggggcag acctgatgta caagatg

47

<210> 311

<211> 47

<212> DNA

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<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-130-58, variant version of SEQ ID234

<221> allele

<222> 24

<223> base T ; C in SEQ ID234

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-130-58.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-130-58.mis2

<210> 312
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<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 99-134-362, variant version of SEQ ID235

<221> allele
<222> 24
<223> base T ; G in SEQ ID235

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-134-362.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-134-362.mis2

<400> 312
caaaacactc atgtagtta gattattatt cctattacaa agataag

47

<210> 313
<211> 47
<212> DNA
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<220>
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<221> allele
<222> 24
<223> base T ; C in SEQ ID236

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-140-130.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-140-130.mis2

<400> 313
tggtcaaaag cagctacaga ccatatgtaa acaattgagc atggctg

47

<210> 314

<220>
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<222> 1..47
<223> polymorphic fragment 99-1462-238, variant version of SEQ ID237

<221> allele
<222> 24
<223> base C ; G in SEQ ID237

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1462-238.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1462-238.mis2

<400> 314
ccctttcaag gttagtaact catctgctgt gtttctgctt cagaagg 47

<210> 315
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 99-147-181, variant version of SEQ ID238

<221> allele
<222> 24
<223> base G ; A in SEQ ID238

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-147-181.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-147-181.mis2

<400> 315
gtgtcatgaa aaagagcatg atagaaagaa aaacttaaat ctttata 47

<210> 316
<211> 47
<212> DNA
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<220>
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<222> 24
<223> base T ; G in SEQ ID239

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1474-156.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1474-156.mis2

<400> 316
cttgactca taagttaaatt attataaca agaagaaata tggactt 47

<210> 317
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 99-1474-359, variant version of SEQ ID240

<221> allele
<222> 24
<223> base G ; A in SEQ ID240

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1474-359.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1474-359.mis2

<400> 317
aaaaaaaaatc aaattattgt accgaattcc ctaatatcag atgtgta 47

<210> 318
<211> 47
<212> DNA
<213> Homo Sapiens

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<223> polymorphic fragment 99-1479-158, variant version of SEQ ID241

<221> allele
<222> 24
<223> base T ; C in SEQ ID241

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1479-158.mis2

<400> 318
tttaaaaatc cacttgtaat cgctgctaattggagtgtat attcagg 47

<210> 319
<211> 47
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<220>
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<223> polymorphic fragment 99-1479-379, variant version of SEQ ID242

<221> allele
<222> 24
<223> base G ; A in SEQ ID242

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1479-379.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1479-379.mis2

<400> 319
gtagagctgt gtactgaggt caggaagca gtcacggta cagcctt 47

<210> 320
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 99-148-129, variant version of SEQ ID243

<221> allele
<222> 24
<223> base G ; A in SEQ ID243

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-129.mis1

<221> primer_bind

ttcatatcta tacaaataat tttgaattta atacataggg ctgcaaaa

47

<210> 321
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<212> DNA
<213> Homo Sapiens

<220>
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<223> polymorphic fragment 99-148-132, variant version of SEQ ID244

<221> allele
<222> 24
<223> base T ; C in SEQ ID244

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-132.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-132.mis2

<400> 321
atatctatac aaataatttt gaatttaata catagggctg caaaaca

47

<210> 322
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 99-148-139, variant version of SEQ ID245

<221> allele
<222> 24
<223> base T ; C in SEQ ID245

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-139.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-139.mis2

<400> 322
tacaaataat tttgaattta atatataggg ctgcaaaaaca aggttga

47

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-148-140, variant version of SEQ ID246

<221> allele

<222> 24

<223> base G ; A in SEQ ID246

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-148-140.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-148-140.mis2

<400> 323

acaaataatt ttgaatttaa tacgtagggc tgcaaaacaa ggttgat

47

<210> 324

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-148-182, variant version of SEQ ID247

<221> allele

<222> 24

<223> base G ; A in SEQ ID247

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-148-182.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-148-182.mis2

<400> 324

ttgatgttga tatgggcaac tgtgtgttgg atggtcccaa agcattc

47

<210> 325

<211> 47

<212> DNA

<213> Homo Sapiens

<221> allele
<222> 24
<223> base T ; G in SEQ ID248

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-366.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-366.mis2

<400> 325
tccttgtaa aggtctctcc ctgttgctca cggctgccgc ctcaaag

47

<210> 326
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-148-76, variant version of SEQ ID249

<221> allele
<222> 24
<223> base T ; C in SEQ ID249

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-76.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-76.mis2

<400> 326
tgatagaatg ccttcctgaa ttattactct tgatggcttc ataaaac

47

<210> 327
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<223> polymorphic fragment 99-1480-290, variant version of SEQ ID250

<221> allele

<222> 1..23
<223> potential microsequencing oligo 99-1480-290.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1480-290.mis2

<400> 327
tgcaccatct tcaccacaac ccctggcaac cactgacct tttactg 47

<210> 328
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-1481-285, variant version of SEQ ID251

<221> allele
<222> 24
<223> base T ; G in SEQ ID251

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1481-285.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1481-285.mis2

<400> 328
tcccataacc tgttttgctt ctctctctaa cctcaagatg gtataaa 47

<210> 329
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 99-1484-101, variant version of SEQ ID252

<221> allele
<222> 24
<223> base C ; A in SEQ ID252

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1484-101.mis1

<400> 329
aaaaagatca aatataagca tgtcactcct ctccttaaaa tctcagt 47

<210> 330
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-1484-328, variant version of SEQ ID253

<221> allele
<222> 24
<223> base C ; G in SEQ ID253

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1484-328.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1484-328.mis2

<400> 330
ggacacgtgg tcatgaggag tttcaaggga ttcagttttc agatccc 47

<210> 331
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-1485-251, variant version of SEQ ID254

<221> allele
<222> 24
<223> base T ; G in SEQ ID254

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1485-251.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1485-251.mis2

<400> 331

<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-1490-381, variant version of SEQ ID255

<221> allele
<222> 24
<223> base T ; C in SEQ ID255

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1490-381.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1490-381.mis2

<400> 332
tgcacagtgg aaataccatg tcatggtacg ctactgtgca tctcttc 47

<210> 333
<211> 47
<212> DNA
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<220>
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<222> 1..47
<223> polymorphic fragment 99-1493-280, variant version of SEQ ID256

<221> allele
<222> 24
<223> base G ; A in SEQ ID256

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1493-280.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1493-280.mis2

<400> 333
ggatgacaga gtattgttgg agggatgggg tttggctgct tggtttt 47

<210> 334
<211> 47
<212> DNA

<222> 1..47
<223> polymorphic fragment 99-151-94, variant version of SEQ ID257

<221> allele
<222> 24
<223> base G ; A in SEQ ID257

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-151-94.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-151-94.mis2

<400> 334
attgagatca ttgataagga aatgttctaa aatttcacaaa tctatat

47

<210> 335
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 99-211-291, variant version of SEQ ID258

<221> allele
<222> 24
<223> base G ; A in SEQ ID258

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-211-291.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-211-291.mis2

<400> 335
ctgggttatat cagactgacc ttctgtgtttt caacagggtca atgcctt

47

<210> 336
<211> 46
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..46
<223> polymorphic fragment 99-213-37, variant version of SEQ ID259

<221> primer_bind
<222> 1..22
<223> potential microsequencing oligo 99-213-37.mis1

<221> primer_bind
<222> 24..46
<223> complement potential microsequencing oligo 99-213-37.mis2

<400> 336
gtgcttccgg ctgcaggact gtgcggagga ctccagtgtc tgacag 46

<210> 337
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 99-221-442, variant version of SEQ ID260

<221> allele
<222> 24
<223> base C ; A in SEQ ID260

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-221-442.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-221-442.mis2

<400> 337
tgcctttgta gatatgcatg ggacttccat gacctagcca gacgaat 47

<210> 338
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-222-109, variant version of SEQ ID261

<221> allele
<222> 24
<223> base T ; C in SEQ ID261

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-222-109.mis2

<400> 338

caggtgagga gtgctggatt ggctacgata tgaatttctt cagcagt

47

<210> 339

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 185, SEQ 262, SEQ 186, SEQ 263, SEQ 187, SEQ 264

<400> 339

tctaacctct catccaac

18

<210> 340

<211> 19

<212> DNA

<213> Homo Sapiens

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<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 188, SEQ 265, SEQ 189, SEQ 266

<400> 340

gttatcgtga gactttttc

19

<210> 341

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 190, SEQ 267, SEQ 191, SEQ 268

<400> 341

tgctggtgct gtgataac

18

<210> 342

<211> 18

<212> DNA

<213> Homo Sapiens

<223> upstream amplification primer for SEQ 192, SEQ 269, SEQ 193, SEQ 270

<400> 342

tacagccctg taagacac

18

<210> 343

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 194, SEQ 271

<400> 343

cagtatgttc aatgcacag

19

<210> 344

<211> 18

<212> DNA

<213> Homo Sapiens

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<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 195, SEQ 272, SEQ 196, SEQ 273

<400> 344

aaaacatcga catgggac

18

<210> 345

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 197, SEQ 274, SEQ 198, SEQ 275, SEQ 199, SEQ 276

<400> 345

agcatttcga gtcatgtg

18

<210> 346

<211> 18

<212> DNA

<213> Homo Sapiens

<400> 346
ccctctttcc tcatgtag 18

<210> 347
<211> 19
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<220>
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<222> 1..19
<223> upstream amplification primer for SEQ 202, SEQ 279, SEQ 203, SEQ 280

<400> 347
taactcgtaa acagagaac 19

<210> 348
<211> 18
<212> DNA
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<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 204, SEQ 281, SEQ 205, SEQ 282, SEQ 206, SEQ 283, SEQ 207, SEQ 284, SEQ 208, SEQ 285

<400> 348
gcgtattgaa gctctttg 18

<210> 349
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 209, SEQ 286, SEQ 210, SEQ 287

<400> 349
aacacgggga ttttaggc 18

<210> 350
<211> 19
<212> DNA
<213> Homo Sapiens

<220>

<400> 350
cacatactaa ggctaattg

19

<210> 351
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 212, SEQ 289, SEQ 213, SEQ 290

<400> 351
gttgctggaa cctatttg

18

<210> 352
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 214, SEQ 291, SEQ 215, SEQ 292

<400> 352
tcgatggctt aatctacc

18

<210> 353
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 216, SEQ 293, SEQ 217, SEQ 294

<400> 353
aaagaggagt aaatgggg

18

<210> 354
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18

<210> 355
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 220, SEQ 297, SEQ 221, SEQ 298

<400> 355
atacctaatt tcaggggg 18

<210> 356
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 222, SEQ 299, SEQ 223, SEQ 300

<400> 356
ttaacagagt accttgag 19

<210> 357
<211> 18
<212> DNA
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<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 224, SEQ 301, SEQ 225, SEQ 302

<400> 357
gtacagcctt ttgcttac 18

<210> 358
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 226, SEQ 303

<210> 359
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 227, SEQ 304

<400> 359
gctgatgagt tagataacc 19

<210> 360
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 228, SEQ 305

<400> 360
aaagccagga ctagaagg 18

<210> 361
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 229, SEQ 306, SEQ 230, SEQ 307,
SEQ 231, SEQ 308, SEQ 232, SEQ 309

<400> 361
gaccagggtt taagttag 18

<210> 362
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 233, SEQ 310

<400> 362

<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 234, SEQ 311

<400> 363
ccataacagc tagtacaac 19

<210> 364
<211> 18
<212> DNA
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<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 235, SEQ 312

<400> 364
tggaaaggta ctcagaag 18

<210> 365
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 236, SEQ 313

<400> 365
agagcatagt ataaagcag 19

<210> 366
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 237, SEQ 314

<400> 366
ctagaagtag cttaacag 19

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 238, SEQ 315

<400> 367

gcagccaatc ttatatattc

19

<210> 368

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 239, SEQ 316, SEQ 240, SEQ 317

<400> 368

aaggttgtag agtagaaag

19

<210> 369

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 241, SEQ 318, SEQ 242, SEQ 319

<400> 369

caactgacac tataaccc

18

<210> 370

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 243, SEQ 320, SEQ 244, SEQ 321, SEQ 245, SEQ 322, SEQ 246, SEQ 323, SEQ 247, SEQ 324, SEQ 248, SEQ 325, SEQ 249, SEQ 326

<400> 370

cagtggagtg tttatgtg

18

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 250, SEQ 327

<400> 371

ttgcacaaaa ggtatagag

19

<210> 372

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 251, SEQ 328

<400> 372

aggctcccct tttgagttg

19

<210> 373

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 252, SEQ 329, SEQ 253, SEQ 330

<400> 373

atcctttcta gctgggag

18

<210> 374

<211> 20

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..20

<223> upstream amplification primer for SEQ 254, SEQ 331

<400> 374

gtttaagaat gtgtgatggg

20

<210> 375

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 255, SEQ 332

<400> 375
aaggcaacag cgttgtgac 19

<210> 376
<211> 18
<212> DNA
<213> Homo Sapiens

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<222> 1..18
<223> upstream amplification primer for SEQ 256, SEQ 333

<400> 376
ttttgggggt tttcagtg 18

<210> 377
<211> 18
<212> DNA
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<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 257, SEQ 334

<400> 377
aacacaacag caaatccc 18

<210> 378
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 258, SEQ 335

<400> 378
tccttacttg taaccccc 18

<210> 379
<211> 20
<212> DNA

<222> 1..20

<223> upstream amplification primer for SEQ 259, SEQ 336

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<223> upstream amplification primer for SEQ 260, SEQ 337

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<210> 381

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<223> upstream amplification primer for SEQ 261, SEQ 338

<400> 381

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<210> 382

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<223> downstream amplification primer for SEQ 185, SEQ 262, SEQ 186, SEQ 263, SEQ 187, SEQ 264

<400> 382

gactgtatcc tttgatgcac

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<210> 383

<211> 20

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<223> downstream amplification primer for SEQ 188, SEQ 265, SEQ 189, SEQ 266

<400> 383

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<210> 384

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<223> downstream amplification primer for SEQ 190, SEQ 267, SEQ 191, SEQ 268

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<223> downstream amplification primer for SEQ 194, SEQ 271

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<400> 387
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SEQ 199, SEQ 276

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<223> downstream amplification primer for SEQ 202, SEQ 279, SEQ 203, SEQ 280

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<210> 391
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<400> 391
aggatcttct acagtcac 18

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<223> downstream amplification primer for SEQ 211, SEQ 288

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<223> downstream amplification primer for SEQ 212, SEQ 289, SEQ 213, SEQ 290

<400> 394
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<400> 396
ctaaggtgtt gtagacag 18

<210> 397
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<400> 397
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<210> 398
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<223> downstream amplification primer for SEQ 220, SEQ 297, SEQ 221, SEQ 298

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<210> 399
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<210> 402
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tattcaqaaa ggagtggg 18

<212> DNA
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SEQ 231, SEQ 308, SEQ 232, SEQ 309

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<400> 405
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<210> 406
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<223> downstream amplification primer for SEQ 234, SEQ 311

<400> 406
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<210> 407
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<223> downstream amplification primer for SEQ 235, SEQ 312

<400> 407
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<213> Homo Sapiens

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<223> downstream amplification primer for SEQ 236, SEQ 313

<400> 408

gaacaacctt gaattagctt g

21

<210> 409

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<212> DNA

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<223> downstream amplification primer for SEQ 237, SEQ 314

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gattccagaa gtccatttca g

21

<210> 410

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<222> 1..21

<223> downstream amplification primer for SEQ 238, SEQ 315

<400> 410

aggtaagaat gagcaaaaag g

21

<210> 411

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<400> 411

gcttgtgttt gttcaattc

19

<210> 412

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<223> downstream amplification primer for SEQ 243, SEQ 320, SEQ 244, SEQ 321, SEQ 245, SEQ 322, SEQ 246, SEQ 323, SEQ 247, SEQ 324, SEQ 248, SEQ 325, SEQ 249, SEQ 326

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<210> 414
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<223> downstream amplification primer for SEQ 250, SEQ 327

<400> 414
ggtgacaggt aaagaaac 18

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<223> downstream amplification primer for SEQ 251, SEQ 328

<400> 415
attcaggcac agaagtcata c 21

<210> 416

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<223> downstream amplification primer for SEQ 252, SEQ 329, SEQ 253, SEQ 330

<400> 416
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<210> 417
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<223> downstream amplification primer for SEQ 254, SEQ 331

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<210> 419
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<223> downstream amplification primer for SEQ 256, SEQ 333

<400> 419
ccttttatatc cttggagtc 19

<210> 420
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<222> 1..21
<223> downstream amplification primer for SEQ 257, SEQ 334

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<223> downstream amplification primer for SEQ 259, SEQ 336

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<400> 423
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<400> 424
gaaacagact gaagcaagga c

21

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tttttgctgt gtcttcaaag tga

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<400> 430
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<400> 434
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<400> 436

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ttccattgt tcctgactt 19

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<210> 439
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<223> microsequencing oligo for 4-42-401.mis1

<400> 441

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23

<210> 442

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<223> potential microsequencing oligo for 4-43-328.mis1

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<210> 443

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cctgagtcctc agggggctga cag 23

<210> 446
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<400> 453
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19

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19

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<400> 458
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<210> 459
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<400> 459
tgactacttt acctgcaata ttt

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<210> 463
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tcaaatacagg acacaccac 19

<210> 465
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<400> 465

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<210> 467
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<210> 468
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cccagaacat tcaccagct 19

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<400> 469
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<400> 471

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19

<210> 472

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<400> 472

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23

<210> 473

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<212> DNA

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<223> potential microsequencing oligo for 99-12907-295.mis1

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tatggcatta tatctccac

19

<210> 474

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<400> 474
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<210> 475
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<400> 475
acactcatgt tagttagat 19

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